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FEATURE:
 NAME/KEY: 3' non-coding sequence
 LOCATION: 1246..2243
 OTHER INFORMATION: /note= "IDENTIFICATION
 OTHER INFORMATION: METHOD-Established by
 OTHER INFORMATION: proximity to location
 OTHER INFORMATION: 1243-1245"
 US-08-474-587-1

Alignment Scores:
 Pred. No.: 5.57 Length: 2243
 Score: 78.00 Matches: 43
 Percent Similarity: 34.638 Conservative: 28
 Best Local Similarity: 20.988 Mismatches: 56
 Query Match: 7.78% Indels: 78
 DB: 1 Gaps: 9

US-09-895-298A-83 (1-190) x US-08-474-587-1 (1-2243)

QY 19 PhePheIlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeu----- 36
 ||||| ||||| :||| ||||| :||| ||||| :||| :|||
 Db 1324 TTGTCATTTTACCTTTTTCRCCGTTTG-GTCTTATGTTATGCCACTG 1380

QY 37 -----AlaIleThrIleTrp-----Arg 42
 :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1381 TAGGTGAAACAGTGTCTGCGTGGCTAACGTTAACGAGTTAGGGCAGCTGTAGT 1440

QY 43 LeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHisserie 62
 ::::: ::::: ::||| :||| :||| :||| :||| :||| :|||
 Db 1441 ATTGAAATGCTATTTGTTCTCTT-----Arg 42
 :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 63 TyrSerTrpIleAspPheIleSerThrArgProGlyTyrLeuTrp-----ValValTrp 80
 ||||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1471 -----CTGTTGAGTAGATGCTGCTGTTGG 1491

QY 81 IleIleArgAsnLeuIleGlySerValHisPhePhePheIleLeuIleLeuIleValLeu 100
 ||||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1492 AAGTATAAGAACG-----TTTTTTTCTCTGCAATTGTGATA 1536

QY 101 IleLeuThrIleLeuIleTrpGlnIleThrGluGlyArgLysIle----- 115
 :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1537 -----AAGAAATTAGTTCTAAAAACCG 1560

QY 116 -----MetIleLeuLeuHisGluGlnIle 124
 :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1561 TCGCACCTTCCCTGAGGCTCTCTGTCGTCGCCAGTGACCCATGGTGGGGTTAGTGTG 1620

QY 125 IleAsnGluIlyLyAspLysMetPheLeuIleGluIlySerIleIlySerGluGlnAspMet 144
 ::||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1621 CTGAGAGATGCTCTGAGAGCATGTACAATGCTGAGAAAGGGAAAGGCCAAAGTCATG 1680

QY 145 GluIysLysIlaAsnProSerSerLeuValLeuGluGuaGargGluValGluGlnGlnGly 164
 ||||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1681 -----ATTCGCCCCATCTCCAAAGTCATATCACAAATCTTGTGGATGCGAAG 1731

QY 165 PheLeuHistGluGlyGluHisAspGlySerLeuAspLeuArgSerArgArgSerValGln 184
 ::::: ::||| :||| :||| :||| :||| :||| :||| :|||
 Db 1732 CACGGATACATGGAGAGTTGAGTAGTGTGATGACCAAGGGCTGGTAAATCCGGT 1791

QY 185 GluGlyAsnProArg 189
 ||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1792 GATTCGAAACGGTGA 1806

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